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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/041,775

DATE: 04/08/2002

TIME: 09:37:41

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\04082002\J041775.raw

ENTERED

3 <110> APPLICANT: BROWN, Eric L.
 4 LEE, Lawrence
 5 HOOK, Magnus
 7 <120> TITLE OF INVENTION: METHOD OF PREVENTING T CELL-MEDIATED RESPONSES BY THE USE OF
 THE MAJOR
 8 HISTOCOMPATIBILITY COMPLEX CLASS II ANALOG PROTEIN (MAP PROTEIN) FROM
 9 STAPHYLOCOCCUS AUREUS
 11 <130> FILE REFERENCE: P07023US01/BAS
 13 <140> CURRENT APPLICATION NUMBER: 10/041,775
 14 <141> CURRENT FILING DATE: 2002-01-10
 16 <150> PRIOR APPLICATION NUMBER: 60/260,523
 17 <151> PRIOR FILING DATE: 2001-01-10
 19 <160> NUMBER OF SEQ ID NOS: 4
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 603
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Staphylococcus aureus
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)..(603)
 31 <223> OTHER INFORMATION:
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 39 aca atc act gtg aat ggt aca agc caa aac att tta tca agc tta aca 96
 40 Thr Ile Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Ser Leu Thr
 41 20 25 30
 43 ttt aat aag aat caa caa att agt tat aaa gat ata gag aat aaa gtt 144
 44 Phe Asn Lys Asn Gln Gln Ile Ser Tyr Lys Asp Ile Glu Asn Lys Val
 45 35 40 45
 47 aaa tca gtt tta tac ttt aat aga ggt att agt gat atc gat tta aga 192
 48 Lys Ser Val Leu Tyr Phe Asn Arg Gly Ile Ser Asp Ile Asp Leu Arg
 49 50 55 60
 51 ctt tct aag caa gca aaa tac acg gtt cat ttt aag aat gga aca aaa 240
 52 Leu Ser Lys Gln Ala Lys Tyr Thr Val His Phe Lys Asn Gly Thr Lys
 53 65 70 75 80
 55 aga gtt gtc gat ttg aaa gca ggc att cac aca gcc gac tta atc aat 288
 56 Arg Val Val Asp Leu Lys Ala Gly Ile His Thr Ala Asp Leu Ile Asn
 57 85 90 95
 59 aca agt gac att aaa gca att agt gtt aac gta gat act aaa aag caa 336
 60 Thr Ser Asp Ile Lys Ala Ile Ser Val Asn Val Asp Thr Lys Lys Gln
 61 100 105 110

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63 gtg aaa gat aaa gag gca aaa gca aat gtt caa gtg ccg tat aca atc      384
64 Val Lys Asp Lys Glu Ala Lys Ala Asn Val Gln Val Pro Tyr Thr Ile
65      115      120      125
67 act gtg aat ggt aca agc caa aac att tta tca aac tta aca ttt aaa      432
68 Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Asn Leu Thr Phe Lys
69      130      135      140
71 aag aat cag caa att agt tat aaa gat tta gag aat aat gta aaa tca      480
72 Lys Asn Gln Gln Ile Ser Tyr Lys Asp Leu Glu Asn Asn Val Lys Ser
73 145      150      155      160
75 gtt tta aaa tca aac aga ggt ata act gat gta gat tta aga ctt tca      528
76 Val Leu Lys Ser Asn Arg Gly Ile Thr Asp Val Asp Leu Arg Leu Ser
77      165      170      175
79 aaa caa gcg aaa ttt aca gtt aat ttt aaa aat ggc acg aaa aaa gtt      576
80 Lys Gln Ala Lys Phe Thr Val Asn Phe Lys Asn Gly Thr Lys Lys Val
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99 Thr Ile Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Ser Leu Thr
100      20      25      30
103 Phe Asn Lys Asn Gln Gln Ile Ser Tyr Lys Asp Ile Glu Asn Lys Val
104      35      40      45
107 Lys Ser Val Leu Tyr Phe Asn Arg Gly Ile Ser Asp Ile Asp Leu Arg
108      50      55      60
111 Leu Ser Lys Gln Ala Lys Tyr Thr Val His Phe Lys Asn Gly Thr Lys
112 65      70      75      80
115 Arg Val Val Asp Leu Lys Ala Gly Ile His Thr Ala Asp Leu Ile Asn
116      85      90      95
119 Thr Ser Asp Ile Lys Ala Ile Ser Val Asn Val Asp Thr Lys Lys Gln
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123 Val Lys Asp Lys Glu Ala Lys Ala Asn Val Gln Val Pro Tyr Thr Ile
124      115      120      125
127 Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Asn Leu Thr Phe Lys
128      130      135      140
131 Lys Asn Gln Gln Ile Ser Tyr Lys Asp Leu Glu Asn Asn Val Lys Ser
132 145      150      155      160
135 Val Leu Lys Ser Asn Arg Gly Ile Thr Asp Val Asp Leu Arg Leu Ser
136      165      170      175
139 Lys Gln Ala Lys Phe Thr Val Asn Phe Lys Asn Gly Thr Lys Lys Val
140      180      185      190
143 Ile Asp Leu Lys Ala Gly Ile Tyr
144      195      200

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153 <221> NAME/KEY: CDS
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155 <223> OTHER INFORMATION:
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163 aca atc act gtg aat ggt aca agc caa aac att tta tca agc tta aca      96
164 Thr Ile Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Ser Leu Thr
165          20          25          30
167 ttt aat aag aat caa caa att agt tat aaa gat ata gag aat aaa gtt      144
168 Phe Asn Lys Asn Gln Gln Ile Ser Tyr Lys Asp Ile Glu Asn Lys Val
169          35          40          45
171 aaa tca gtt tta tac ttt aat aga ggt att agt gat atc gat tta aga      192
172 Lys Ser Val Leu Tyr Phe Asn Arg Gly Ile Ser Asp Ile Asp Leu Arg
173          50          55          60
175 ctt tct aag caa gca aaa tac acg gtt cat ttt aag aat gga aca aaa      240
176 Leu Ser Lys Gln Ala Lys Tyr Thr Val His Phe Lys Asn Gly Thr Lys
177 65          70          75          80
179 aga gtt gtc gat ttg aaa gca ggc att cac aca gcc gac tta atc aat      288
180 Arg Val Val Asp Leu Lys Ala Gly Ile His Thr Ala Asp Leu Ile Asn
181          85          90          95
183 aca agt gac att aaa gca att agt gtt aac gta gat act aaa aag caa      336
184 Thr Ser Asp Ile Lys Ala Ile Ser Val Asn Val Asp Thr Lys Lys Gln
185          100          105          110
187 gtg aaa gat aaa gag gca aaa gca aat gtt gtc gac ctg cag cca agc      384
188 Val Lys Asp Lys Glu Ala Lys Ala Asn Val Val Asp Leu Gln Pro Ser
189          115          120          125
191 tta att agc tga      396
192 Leu Ile Ser
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208          20          25          30
211 Phe Asn Lys Asn Gln Gln Ile Ser Tyr Lys Asp Ile Glu Asn Lys Val
212          35          40          45
215 Lys Ser Val Leu Tyr Phe Asn Arg Gly Ile Ser Asp Ile Asp Leu Arg
216          50          55          60

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219 Leu Ser Lys Gln Ala Lys Tyr Thr Val His Phe Lys Asn Gly Thr Lys
220 65          70          75          80
223 Arg Val Val Asp Leu Lys Ala Gly Ile His Thr Ala Asp Leu Ile Asn
224          85          90          95
227 Thr Ser Asp Ile Lys Ala Ile Ser Val Asn Val Asp Thr Lys Lys Gln
228          100          105          110
231 Val Lys Asp Lys Glu Ala Lys Ala Asn Val Val Asp Leu Gln Pro Ser
232          115          120          125
235 Leu Ile Ser
236          130

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VERIFICATION SUMMARY

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